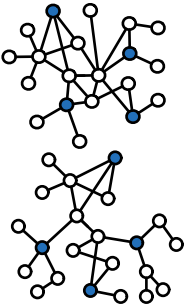
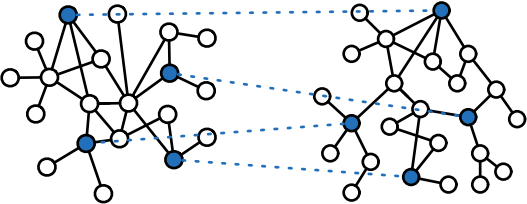


**Landmark Selection:**

We choose a set of landmarks from known homologs.



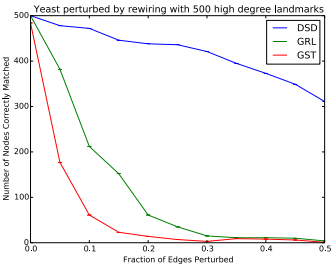
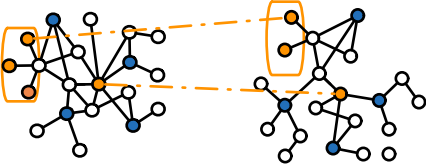
**Distance Vectors:**

For every vertex in each graph, a vector of distances to landmarks is created. The inner product is used to define a distance between genes across networks

Network 1	Network 2
$u1 <3, 4, 2, 2>$	$v1 <3, 2, 2, 1>$
$u2 <2, 5, 2, 1>$	$v2 <4, 3, 2, 1>$
$d(u1,u2) = 28$	

**Matching:**

We identify automorphisms and match at the orbit level using a modified Hungarian and our new method ReciprocalRank. We introduce a new validation technique using a cross-validation of known homologs.



**Results:**

We compare our method against competing techniques on a battery of tests.